Jinn-Moon Yang

List of Publications by Year
in descending order

150 papers	4,151 citations	147566 31 h-index	128067 60 g-index
153 all docs	153 docs citations	153 times ranked	5627 citing authors

#	Article	IF	Citations
1	GEMDOCK: A generic evolutionary method for molecular docking. Proteins: Structure, Function and Bioinformatics, 2004, 55, 288-304.	1.5	519
2	iGEMDOCK: a graphical environment of enhancing GEMDOCK using pharmacological interactions and post-screening analysis. BMC Bioinformatics, 2011, 12, S33.	1.2	335
3	Consensus Scoring Criteria for Improving Enrichment in Virtual Screening. Journal of Chemical Information and Modeling, 2005, 45, 1134-1146.	2.5	220
4	The cAMP Receptor-Like Protein CLP Is a Novel c-di-GMP Receptor Linking Cellâ€“Cell Signaling to Virulence Gene Expression in Xanthomonas campestris. Journal of Molecular Biology, 2010, 396, 646-662.	2.0	191
5	(PS)2: protein structure prediction server. Nucleic Acids Research, 2006, 34, W152-W157.	6.5	123
6	An Evolutionary Algorithm for Large Traveling Salesman Problems. IEEE Transactions on Systems, Man, and Cybernetics, 2004, 34, 1718-1729.	5.5	101
7	(PS)2-v2: template-based protein structure prediction server. BMC Bioinformatics, 2009, 10, 366.	1.2	101
8	Protein structure database search and evolutionary classification. Nucleic Acids Research, 2006, 34, 3646-3659.	6.5	99
9	Aurintricarboxylic acid inhibits influenza virus neuraminidase. Antiviral Research, 2009, 81, 123-131.	1.9	93
10	PhosphoPOINT: a comprehensive human kinase interactome and phospho-protein database. Bioinformatics, 2008, 24, i14-i20.	1.8	88
11	A pharmacophore-based evolutionary approach for screening selective estrogen receptor modulators. Proteins: Structure, Function and Bioinformatics, 2005, 59, 205-220.	1.5	87
12	Combinatorial Computational Approaches to Identify Tetracycline Derivatives as Flavivirus Inhibitors. PLoS ONE, 2007, 2, e428.	1.1	87
13	KDM4B as a Target for Prostate Cancer: Structural Analysis and Selective Inhibition by a Novel Inhibitor. Journal of Medicinal Chemistry, 2014, 57, 5975-5985.	2.9	85
14	Crystal structure of a secondary vitamin D₃ binding site of milk Î²â€lactoglobulin. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1197-1210.	1.5	79
15	Kappa-alpha plot derived structural alphabet and BLOSUM-like substitution matrix for rapid search of protein structure database. Genome Biology, 2007, 8, R31.	13.9	73
16	Applying family competition to evolution strategies for constrained optimization. Lecture Notes in Computer Science, 1997, , 201-211.	1.0	67
17	Membrane protein-regulated networks across human cancers. Nature Communications, 2019, 10, 3131.	5.8	67
18	Development and evaluation of a generic evolutionary method for protein-ligand docking. Journal of Computational Chemistry, 2004, 25, 843-857.	1.5	58

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19	Relationship between protein structures and disulfide-bonding patterns. Proteins: Structure, Function and Bioinformatics, 2003, 53, 1-5.	1.5	54
20	Crowning Proteins: Modulating the Protein Surface Properties using Crown Ethers. Angewandte Chemie - International Edition, 2014, 53, 13054-13058.	7.2	49
21	Flexible ligand docking using a robust evolutionary algorithm. Journal of Computational Chemistry, 2000, 21, 988-998.	1.5	46
22	DNA Mimic Proteins: Functions, Structures, and Bioinformatic Analysis. Biochemistry, 2014, 53, 2865-2874.	1.2	46
23	3D-partner: a web server to infer interacting partners and binding models. Nucleic Acids Research, 2007, 35, W561-W567.	6.5	45
24	The inhibitory effects of PGG and EGCG against the SARS-CoV-2 3C-like protease. Biochemical and Biophysical Research Communications, 2022, 591, 130-136.	1.0	41
25	Co-evolution positions and rules for antigenic variants of human influenza A/H3N2 viruses. BMC Bioinformatics, 2009, 10, S41.	1.2	38
26	Uncovering Flexible Active Site Conformations of SARS-CoV-2 3CL Proteases through Protease Pharmacophore Clusters and COVID-19 Drug Repurposing. ACS Nano, 2021, 15, 857-872.	7.3	38
27	SiMMap: a web server for inferring site-moiety map to recognize interaction preferences between protein pockets and compound moieties. Nucleic Acids Research, 2010, 38, W424-W430.	6.5	37
28	A Robust Evolutionary Algorithm for Training Neural Networks. Neural Computing and Applications, 2001, 10, 214-230.	3.2	36
29	Novel Class IIa-Selective Histone Deacetylase Inhibitors Discovered Using an in Silico Virtual Screening Approach. Scientific Reports, 2017, 7, 3228.	1.6	36
30	PPISearch: a web server for searching homologous proteinâ€“protein interactions across multiple species. Nucleic Acids Research, 2009, 37, W369-W375.	6.5	34
31	3D-interologs: an evolution database of physical protein- protein interactions across multiple genomes. BMC Genomics, 2010, 11, S7.	1.2	34
32	PAComplex: a web server to infer peptide antigen families and binding models from TCRâ€“pMHC complexes. Nucleic Acids Research, 2011, 39, W254-W260.	6.5	34
33	Synthesis of acylguanidine zanamivir derivatives as neuraminidase inhibitors and the evaluation of their bio-activities. Organic and Biomolecular Chemistry, 2013, 11, 3943.	1.5	32
34	Staphylococcus aureus protein SAUGI acts as a uracil-DNA glycosylase inhibitor. Nucleic Acids Research, 2014, 42, 1354-1364.	6.5	32
35	Changed epitopes drive the antigenic drift for influenza A (H3N2) viruses. BMC Bioinformatics, 2011, 12, S31.	1.2	30
36	Module organization and variance in protein-protein interaction networks. Scientific Reports, 2015, 5, 9386.	1.6	30

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37	Repurposing existing drugs: identification of SARS-CoV-2 3C-like protease inhibitors. Journal of Enzyme Inhibition and Medicinal Chemistry, 2021, 36, 147-153.	2.5	29
38	Fine-grained protein fold assignment by support vector machines using generalized npeptide coding schemes and jury voting from multiple-parameter sets. Proteins: Structure, Function and Bioinformatics, 2003, 50, 531-536.	1.5	28
39	Rational Design for Crystallization of Î²-Lactoglobulin and Vitamin D₃ Complex: Revealing a Secondary Binding Site. Crystal Growth and Design, 2008, 8, 4268-4276.	1.4	27
40	Structures of Helicobacter pylori Shikimate Kinase Reveal a Selective Inhibitor-Induced-Fit Mechanism. PLoS ONE, 2012, 7, e33481.	1.1	27
41	Design and synthesis of 1,2,3-triazole-containing N -acyl zanamivir analogs as potent neuraminidase inhibitors. European Journal of Medicinal Chemistry, 2016, 123, 397-406.	2.6	26
42	Nicotinic Acetylcholine Receptor Subtype Alpha-9 Mediates Triple-Negative Breast Cancers Based on a Spontaneous Pulmonary Metastasis Mouse Model. Frontiers in Cellular Neuroscience, 2017, 11, 336.	1.8	25
43	Novel Lactulose and Melibiose Targeting Autophagy to Reduce PolyQ Aggregation in Cell Models of Spinocerebellar Ataxia 3. CNS and Neurological Disorders - Drug Targets, 2016, 15, 351-359.	0.8	24
44	KIDFamMap: a database of kinase-inhibitor-disease family maps for kinase inhibitor selectivity and binding mechanisms. Nucleic Acids Research, 2013, 41, D430-D440.	6.5	23
45	Some issues of designing genetic algorithms for traveling salesman problems. Soft Computing, 2004, 8, 689-697.	2.1	22
46	fastSCOP: a fast web server for recognizing protein structural domains and SCOP superfamilies. Nucleic Acids Research, 2007, 35, W438-W443.	6.5	22
47	Pathway-based Screening Strategy for Multitarget Inhibitors of Diverse Proteins in Metabolic Pathways. PLoS Computational Biology, 2013, 9, e1003127.	1.5	22
48	GEM: A Gaussian evolutionary method for predicting protein side-chain conformations. Protein Science, 2002, 11, 1897-1907.	3.1	21
49	The potential of lactulose and melibiose, two novel trehalase-indigestible and autophagy-inducing disaccharides, for polyQ-mediated neurodegenerative disease treatment. NeuroToxicology, 2015, 48, 120-130.	1.4	21
50	An evolutionary algorithm for the synthesis of multilayer coatings at oblique light incidence. Journal of Lightwave Technology, 2001, 19, 559-570.	2.7	20
51	Antigenic sites of H1N1 influenza virus hemagglutinin revealed by natural isolates and inhibition assays. Vaccine, 2012, 30, 6327-6337.	1.7	20
52	Core Site-Moiety Maps Reveal Inhibitors and Binding Mechanisms of Orthologous Proteins by Screening Compound Libraries. PLoS ONE, 2012, 7, e32142.	1.1	20
53	Solving traveling salesman problems by combining global and local search mechanisms. , 0, , .		19
54	An Evolutionary Approach for Gene Expression Patterns. IEEE Transactions on Information Technology in Biomedicine, 2004, 8, 69-78.	3.6	19

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55	7-Chloro-6-piperidin-1-yl-quinoline-5,8-dione (PT-262), a novel ROCK inhibitor blocks cytoskeleton function and cell migration. Biochemical Pharmacology, 2011, 81, 856-865.	2.0	19
56	Identification of Inhibitors for the DEDDh Family of Exonucleases and a Unique Inhibition Mechanism by Crystal Structure Analysis of CRN-4 Bound with 2-Morpholin-4-ylethanesulfonate (MES). Journal of Medicinal Chemistry, 2016, 59, 8019-8029.	2.9	19
57	Structural simulation and protein engineering to convert an endo-chitosanase to an exo-chitosanase. Protein Engineering, Design and Selection, 2008, 21, 561-566.	1.0	18
58	Omics-based Investigation of Diet-induced Obesity Synergized with HBx, Src, and p53 Mutation Accelerating Hepatocarcinogenesis in Zebrafish Model. Cancers, 2019, 11, 1899.	1.7	18
59	Efficient evolutionary algorithm for the thin-film synthesis of inhomogeneous optical coatings. Applied Optics, 2001, 40, 3256.	2.1	17
60	CRISPR/Cas9 Genome Editing of Epidermal Growth Factor Receptor Sufficiently Abolished Oncogenicity in Anaplastic Thyroid Cancer. Disease Markers, 2018, 2018, 1-14.	0.6	17
61	A combined evolutionary algorithm for real parameters optimization. , 0, , .		16
62	A family competition evolutionary algorithm for automated docking of flexible ligands to proteins. IEEE Transactions on Information Technology in Biomedicine, 2000, 4, 225-237.	3.6	16
63	5-Demethyltangeretin is more potent than tangeretin in inhibiting dimethylbenz(a)anthracene (DMBA)/12-O-tetradecanoylphorbol-13-acetate (TPA)-induced skin tumorigenesis. Journal of Functional Foods, 2014, 11, 528-537.	1.6	16
64	Pharmacophore anchor models of flaviviral NS3 proteases lead to drug repurposing for DENV infection. BMC Bioinformatics, 2017, 18, 548.	1.2	16
65	Zika Virus NS3 Protease Pharmacophore Anchor Model and Drug Discovery. Scientific Reports, 2020, 10, 8929.	1.6	16
66	A GENETIC ALGORITHM WITH ADAPTIVE MUTATIONS AND FAMILY COMPETITION FOR TRAINING NEURAL NETWORKS. International Journal of Neural Systems, 2000, 10, 333-352.	3.2	15
67	Heterogeneous Selection Genetic Algorithms For Traveling Salesman Problems. Engineering Optimization, 2003, 35, 297-311.	1.5	15
68	MoNetFamily: a web server to infer homologous modules and moduleâ€“module interaction networks in vertebrates. Nucleic Acids Research, 2012, 40, W263-W270.	6.5	15
69	Identification of neuraminidase inhibitors against dual H274Y/I222R mutant strains. Scientific Reports, 2017, 7, 12336.	1.6	14
70	CAPIH: A Web interface for comparative analyses and visualization of host-HIV protein-protein interactions. BMC Microbiology, 2009, 9, 164.	1.3	13
71	Roles of Amino Acids in the Escherichia coli Octaprenyl Diphosphate Synthase Active Site Probed by Structure-Guided Site-Directed Mutagenesis. Biochemistry, 2012, 51, 3412-3419.	1.2	13
72	Genome-wide structural modelling of TCR-pMHC interactions. BMC Genomics, 2013, 14, S5.	1.2	13

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73	An evolutionary algorithm for synthesizing optical thin-film designs. Lecture Notes in Computer Science, 1998, , 947-956.	1.0	12
74	PCFamily: a web server for searching homologous protein complexes. Nucleic Acids Research, 2010, 38, W516-W522.	6.5	12
75	Deep learning with evolutionary and genomic profiles for identifying cancer subtypes. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940005.	0.3	12
76	Loss of Fis1 impairs proteostasis during skeletal muscle aging in Drosophila. Aging Cell, 2021, 20, e13379.	3.0	12
77	Anchor-based classification and type-C inhibitors for tyrosine kinases. Scientific Reports, 2015, 5, 10938.	1.6	11
78	Ugonin J Acts as a SARS-CoV-2 3C-like Protease Inhibitor and Exhibits Anti-inflammatory Properties. Frontiers in Pharmacology, 2021, 12, 720018.	1.6	11
79	Total Synthetic Protoapigenone <scp>WYC</scp>02 Inhibits Cervical Cancer Cell Proliferation and Tumour Growth through <scp>PIK</scp>3 Signalling Pathway. Basic and Clinical Pharmacology and Toxicology, 2013, 113, 8-18.	1.2	10
80	Parallel Screening of Wild-Type and Drug-Resistant Targets for Anti-Resistance Neuraminidase Inhibitors. PLoS ONE, 2013, 8, e56704.	1.1	10
81	Optical Coating Designs Using the Family Competition Evolutionary Algorithm. Evolutionary Computation, 2001, 9, 421-443.	2.3	9
82	Alternative splicing in human cancer cells is modulated by the amiloride derivative 3,5â€diaminoâ€6â€chloroâ€Nâ€(Nâ€(2,6â€dichlorobenzoyl)carbamimidoyl)pyrazineâ€2â€carboxide. Molecular Oncology, 2019, 13, 1744-1762.	2.1	9
83	Reconstructing Genome-Wide Proteinâ€“Protein Interaction Networks Using Multiple Strategies with Homologous Mapping. PLoS ONE, 2015, 10, e0116347.	1.1	8
84	Management of different kinds of head and neck defects with the submental flap for reconstruction. European Archives of Oto-Rhino-Laryngology, 2015, 272, 3815-3819.	0.8	8
85	Convolutional neural network for human cancer types prediction by integrating protein interaction networks and omics data. Scientific Reports, 2021, 11, 20691.	1.6	8
86	LigSeeSVM: Ligand-based virtual Screening using Support Vector Machines and data fusion. International Journal of Computational Biology and Drug Design, 2011, 4, 274.	0.3	7
87	Steric recognition of Tâ€cell receptor contact residues is required to map mutant epitopes by immunoinformatical programmes. Immunology, 2012, 136, 139-152.	2.0	7
88	Moiety-Linkage Map Reveals Selective Nonbisphosphonate Inhibitors of Human Geranylgeranyl Diphosphate Synthase. Journal of Chemical Information and Modeling, 2013, 53, 2299-2311.	2.5	7
89	Homopharma: A new concept for exploring the molecular binding mechanisms and drug repurposing. BMC Genomics, 2014, 15, S8.	1.2	7
90	A site-moiety map and virtual screening approach for discovery of novel 5-LOX inhibitors. Scientific Reports, 2020, 10, 10510.	1.6	7

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91	DAPID: a 3D-domain annotated protein-protein interaction database. Genome Informatics, 2006, 17, 206-15.	0.4	7
92	Vascular anatomy is a determining factor of successful submental flap raising: a retrospective study of 70 clinical cases. PeerJ, 2017, 5, e3606.	0.9	6
93	A robust evolutionary algorithm for optical thin-film designs. , 0, , .		5
94	Consensus scoring criteria in structure-based virtual screening. , 0, , .		5
95	Evolutionary conservation of DNA-contact residues in DNA-binding domains. BMC Bioinformatics, 2008, 9, S3.	1.2	5
96	Evaluating Instantaneous Perfusion Responses of Parotid Glands to Gustatory Stimulation Using High-Temporal-Resolution Echo-Planar Diffusion-Weighted Imaging. American Journal of Neuroradiology, 2016, 37, 1909-1915.	1.2	5
97	An integrated approach with new strategies for QSAR models and lead optimization. BMC Genomics, 2017, 18, 104.	1.2	5
98	A new evolutionary approach to developing neural autonomous agents. , 0, , .		4
99	Space-related pharma-motifs for fast search of protein binding motifs and polypharmacological targets. BMC Genomics, 2012, 13, S21.	1.2	4
100	Inferring homologous protein-protein interactions through pair position specific scoring matrix. BMC Bioinformatics, 2013, 14, S11.	1.2	4
101	Target Identification Using Homopharma and Network-Based Methods for Predicting Compounds Against Dengue Virus-Infected Cells. Molecules, 2020, 25, 1883.	1.7	4
102	An integrated systematic approach for investigating microcurrent electrical nerve stimulation (MENS) efficacy in STZ-induced diabetes mellitus. Life Sciences, 2021, 279, 119650.	2.0	4
103	A Nanodiamond-Based Surface Topography Downregulates the MicroRNA miR6236 to Enhance Neuronal Development and Regeneration. ACS Applied Bio Materials, 2021, 4, 890-902.	2.3	4
104	A robust evolutionary algorithm for global optimization. Engineering Optimization, 2002, 34, 405-425.	1.5	3
105	Modeling the Binding and Inhibition Mechanism of Nucleotides and Sulfotransferase Using Molecular Docking. Journal of the Chinese Chemical Society, 2003, 50, 655-663.	0.8	3
106	Binding Affinity Analysis of Protein-Ligand Complexes. , 2008, , .		3
107	TSCC: Two-Stage Combinatorial Clustering for virtual screening using protein-ligand interactions and physicochemical features. BMC Genomics, 2010, 11, S26.	1.2	3
108	GemAffinity: a scoring function for predicting binding affinity and Virtual Screening. International Journal of Data Mining and Bioinformatics, 2012, 6, 27.	0.1	3

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109	Clinical assessment of diode laser-assisted endoscopic intrasphenoidal vidian neurectomy in the treatment of refractory rhinitis. Lasers in Medical Science, 2017, 32, 2097-2104.	1.0	3
110	Identification of the PCA29 gene signature as a predictor in prostate cancer. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940006.	0.3	3
111	Can Face- and Smartphone-Touching Behaviors Be Altered with Personal Hygiene Reminders during the COVID-19 Pandemic Period? An Observational Study. International Journal of Environmental Research and Public Health, 2021, 18, 10038.	1.2	3
112	Furin and TMPRSS2 Resistant Spike Induces Robust Humoral and Cellular Immunity Against SARS-CoV-2 Lethal Infection. Frontiers in Immunology, 2022, 13, 872047.	2.2	3
113	Integrating adaptive mutations and family competition with differential evolution for flexible ligand docking. , 0, , .		2
114	An Evolutionary Approach with Pharmacophore-Based Scoring Functions for Virtual Database Screening. Lecture Notes in Computer Science, 2004, , 481-492.	1.0	2
115	ATRIPPI: AN ATOM-RESIDUE PREFERENCE SCORING FUNCTION FOR PROTEINâ€“PROTEIN INTERACTIONS. International Journal on Artificial Intelligence Tools, 2010, 19, 251-266.	0.7	2
116	Diode laser assisted minimal invasive sphenoidotomy for endoscopic transphenoidal pituitary surgery: Our technique and results. Lasers in Surgery and Medicine, 2015, 47, 239-242.	1.1	2
117	Finding Influential Genes Using Gene Expression Data and Boolean Models of Metabolic Networks. , 2016, , .		2
118	Boolean function network analysis of time course liver transcriptome data to reveal novel circadian transcriptional regulators in mammals. Journal of the Chinese Medical Association, 2019, 82, 872-880.	0.6	2
119	An Integrated Genomic Strategy to Identify CHRNB4 as a Diagnostic/Prognostic Biomarker for Targeted Therapy in Head and Neck Cancer. Cancers, 2020, 12, 1324.	1.7	2
120	Pharmacophore anchor models of ATAT1 to discover potential inhibitors and lead optimization. Computational Biology and Chemistry, 2021, 93, 107513.	1.1	2
121	Identification of pan-kinase-family inhibitors using graph convolutional networks to reveal family-sensitive pre-moieties. BMC Bioinformatics, 2022, 23, .	1.2	2
122	Exploring kinase family inhibitors and their moiety preferences using deep SHapley additive exPlanations. BMC Bioinformatics, 2022, 23, .	1.2	2
123	Incorporation family competition into Gaussian and Cauchy mutations to training neural networks using an evolutionary algorithm. , 0, , .		1
124	An evolutionary algorithm for the synthesis of oblique incidence optical coatings. , 0, , .		1
125	GEMSCORE: A New Empirical Energy Function for Protein Folding. , 2005, , .		1
126	Clinical application of suction-tube-assisted septal submucosal dissection for endoscopic septoplasty. European Archives of Oto-Rhino-Laryngology, 2017, 274, 1471-1475.	0.8	1

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127	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. BMC Systems Biology, 2018, 12, 13.	3.0	1
128	Deep Learning with Evolutionary and Genomic Profiles for Identifying Cancer Subtypes. , 2018, , .		1
129	An Evolutionary Approach for Molecular Docking. Lecture Notes in Computer Science, 2003, , 2372-2383.	1.0	1
130	FooDisNET: a database of food-compound-protein-disease associations. , 2020, , .		1
131	Discovery of moiety preference by Shapley value in protein kinase family using random forest models. BMC Bioinformatics, 2022, 23, 130.	1.2	1
132	GEMPLS: A New QSAR Method Combining Generic Evolutionary Method and Partial Least Squares. Lecture Notes in Computer Science, 2005, , 125-135.	1.0	0
133	Evolutionary conservation of DNA-contact residues in DNA-binding domains. , 2007, , .		0
134	Soft energy function and generic evolutionary method for discriminating native from nonnative protein conformations. Journal of Computational Chemistry, 2008, 29, 1364-1373.	1.5	0
135	Evolutionary Conservation and Interacting Preference for Identifying Protein-DNA Interactions. , 2008, , .		0
136	Identifying Critical Positions and Rules of Antigenic Drift for Influenza A/H3N2 Viruses. , 2008, , .		0
137	3D-interologs: A Protein-Protein Interacting Evolution Database across Multiple Species. , 2009, , .		0
138	ATRIPPI: An Atom-residue Preference Scoring Function for Protein-protein Interactions. , 2009, , .		0
139	GemAffinity: A Scoring Function for Predicting Binding Affinity and Virtual Screening. , 2009, , .		0
140	Template-based scoring functions for visualizing biological insights of H-2K^b-peptide-TCR complexes. , 2010, , .		0
141	The Relevance of Protein-Ligand Interaction Profiles in Computer-Aided Novel Compound Design and Applications. Current Bioinformatics, 2011, 6, 383-388.	0.7	0
142	Steric recognition of T-cell receptor contact residues is required to map mutant epitopes by immunoinformatical programmes. Immunology, 2012, 136, 459-459.	2.0	0
143	Rank-based interolog mapping for predicting proteinprotein interactions between genomes. , 2013, , .		0
144	Template-based scoring functions for visualising biological insights of H-2K^b-peptide-TCR complexes. International Journal of Data Mining and Bioinformatics, 2013, 8, 326.	0.1	0

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145	Identification of the PCa28 Gene Signature as a Predictor in Prostate Cancer. , 2018, , .		0
146	Flexible Ligand Docking Using a Robust Evolutionary Algorithm. , 2000, , 95-106.		0
147	A Gaussian Evolutionary Method for Predicting Protein-Protein Interaction Sites. , 2007, , 143-154.		0
148	Configurational Differences and Binding Mechanisms of Interleukin-1 Receptor-Associated Kinase 1. , 2020, , .		0
149	CoMI: consensus mutual information for tissue-specific gene signatures. BMC Bioinformatics, 2021, 22, 624.	1.2	0
150	Evolutionary Conservation of DNA-Contact residues in DNA-bindingDomains. , 2007, , .		0